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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/002,050

DATE: 04/17/2002
 TIME: 14:19:50

Input Set : A:\EP.txt
 Output Set: N:\CRF3\04172002\J002050.raw

3 <110> APPLICANT: Shimkets, Richard
 4 Fernandes, Elma
 5 Vernet, Corine
 6 Yang, Meijia
 7 Boldog, Ferenc
 8 Herrmann, John
 10 <120> TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Human Semaphorin-Like Polypeptides
 12 <130> FILE REFERENCE: 15966-554 Cura-54 CON-S14
 14 <140> CURRENT APPLICATION NUMBER: 10/002,050
 15 <141> CURRENT FILING DATE: 2001-11-02
 17 <150> PRIOR APPLICATION NUMBER: 09/604,286
 18 <151> PRIOR FILING DATE: 2000-06-22
 20 <150> PRIOR APPLICATION NUMBER: 60/140,584
 21 <151> PRIOR FILING DATE: 1999-06-23
 23 <160> NUMBER OF SEQ ID NOS: 49
 25 <170> SOFTWARE: PatentIn Ver. 2.0
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 28 <211> LENGTH: 932
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
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 34 <222> LOCATION: (113)..(793)
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 39 Met Gly
 40 1
 42 tgg aca atg agg ctg gtc aca gca gca ctg tta ctg ggt ctc atg atg 166
 43 Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu Met Met
 44 5 10 15
 46 gtg gtc act gga gac gag gat gag aac agc ccg tgt gcc cat gag gcc 214
 47 Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His Glu Ala
 48 20 25 30
 50 ctc ttg gac gag gac acc ctc ttt tgc cag ggc ctt gaa gtt ttc tac 262
 51 Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val Phe Tyr
 52 35 40 45 50
 54 cca gag ttg ggg aac att ggc tgc aag gtt gtt cct gat tgt aac aac 310
 55 Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys Asn Asn
 56 55 60 65
 58 tac aga cag aag atc acc tcc tgg atg gag ccg ata gtc aag ttc ccg 358
 59 Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys Phe Pro
 60 70 75 80

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62 ggg gcc gtg gac ggc gca acc tat atc ctg gtg atg gtg gat cca gat 406
63 Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp Pro Asp
64      85      90      95
66 gcc cct agc aga gca gaa ccc aga cag aga ttc tgg aga cat tgg ctg 454
67 Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His Trp Leu
68      100      105      110
70 gta aca gat atc aag ggc gcc gac ctg aag gaa ggg aag att cag ggc 502
71 Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Glu Gly Lys Ile Gln Gly
72      115      120      125      130
74 cag gag tta tca gcc tac cag gct ccc tcc cca ccg gca cac agt ggc 550
75 Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly
76      135      140      145
78 ttc cat cgc tac cag ttc ttt gtc tat ctt cag gaa gga aaa gtc atc 598
79 Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile
80      150      155      160
82 tct ctc ctt ccc aag gaa aac aaa act cga ggc tct tgg aaa atg gac 646
83 Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp
84      165      170      175
86 aga ttt ctg aac cgt ttc cac ctg ggc gaa cct gaa gca agc acc cag 694
87 Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln
88      180      185      190
90 ttc atg acc cag aac tac cag gac tca cca acc ctc cag gct ccc aga 742
91 Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg
92      195      200      205      210
94 gaa agg gcc agc gag ccc aag cac aaa aac cag gcg gag ata gct gcc 790
95 Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile Ala Ala
96      215      220      225
98 tgc tagatagccg gctttgccat ccgggcatgt ggccacactg cccaccaccg 843
99 Cys
101 acgatgtggg tatggaaccc cctctggata cagaaccctt tcttttccaa attaaaaaaa 903
103 aaaatcatcc aggaaaaaaa aaaaaaaaaa 932
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107 <211> LENGTH: 227
108 <212> TYPE: PRT
109 <213> ORGANISM: Homo sapiens
111 <400> SEQUENCE: 2
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115 Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
116      20      25      30
118 Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
119      35      40      45
121 Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
122      50      55      60
124 Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
125      65      70      75      80
127 Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
128      85      90      95
130 Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His

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131          100          105          110
133 Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Glu Gly Lys Ile
134          115          120          125
136 Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
137          130          135          140
139 Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
140 145          150          155          160
142 Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
143          165          170          175
145 Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
146          180          185          190
148 Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
149          195          200          205
151 Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
152          210          215          220
154 Ala Ala Cys
155 225
158 <210> SEQ ID NO: 3
159 <211> LENGTH: 734
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapiens
163 <220> FEATURE:
164 <221> NAME/KEY: CDS
165 <222> LOCATION: (66)..(734)
167 <400> SEQUENCE: 3
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170 cagtc atg gtg cga acg cgg tgg cag cct cac cct ccg ccg ccc ctg ctt 110
171 Met Val Arg Thr Arg Trp Gln Pro His Pro Pro Pro Pro Leu Leu
172          1          5          10          15
174 ctc ctg gtg ctc gtg tgg ctc ccc caa agc ctg agt cta gac ctg att 158
175 Leu Leu Val Leu Val Trp Leu Pro Gln Ser Leu Ser Leu Asp Leu Ile
176          20          25          30
178 gcc tac gtg ccg cag ata aca gcc tgg gac ctg gaa ggg aag atc aca 206
179 Ala Tyr Val Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Ile Thr
180          35          40          45
182 gcc act aca ttc tct ctg gag cag cct cgg tgc gtc ttt gat gag cat 254
183 Ala Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Glu His
184          50          55          60
186 gtc tca act aag gac acc atc tgg cta gtg gtg gct ttc agc aat gcc 302
187 Val Ser Thr Lys Asp Thr Ile Trp Leu Val Val Ala Phe Ser Asn Ala
188          65          70          75
190 tcc agg gac ttt cag aac cca cag act gct gct aag atc ccg acc ttc 350
191 Ser Arg Asp Phe Gln Asn Pro Gln Thr Ala Ala Lys Ile Pro Thr Phe
192 80          85          90          95
194 cca cag ctg ctg act gac ggc cac tat atg aca tta ccc ctg tcc ctg 398
195 Pro Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Leu
196          100          105          110
198 gat cag ctg cca tgt gag gac ctg acc ggt ggc agt gga ggt gtc ccc 446
199 Asp Gln Leu Pro Cys Glu Asp Leu Thr Gly Gly Ser Gly Gly Val Pro

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200          115          120          125
202 gtg ctt cgg gtg ggc aat gat ttt ggc tgt tac cag cga ccc tat tgc 494
203 Val Leu Arg Val Gly Asn Asp Phe Gly Cys Tyr Gln Arg Pro Tyr Cys
204          130          135          140
206 aac gcc ccc ctc ccc agc cag ggc cct tac agt gtg aag ttc ctt gta 542
207 Asn Ala Pro Leu Pro Ser Gln Gly Pro Tyr Ser Val Lys Phe Leu Val
208          145          150          155
210 atg gat gcc gcc ggc cca ccc aag gct gag acg aag tgg tcc aac ccc 590
211 Met Asp Ala Ala Gly Pro Pro Lys Ala Glu Thr Lys Trp Ser Asn Pro
212 160          165          170          175
214 att tat ctc cac caa gga aag aat ccc aac tcc att gac aca tgg cct 638
215 Ile Tyr Leu His Gln Gly Lys Asn Pro Asn Ser Ile Asp Thr Trp Pro
216          180          185          190
218 ggc cga cgg agc ggc tgt atg atc gtc ata act tcc atc ctc tct gcc 686
219 Gly Arg Arg Ser Gly Cys Met Ile Val Ile Thr Ser Ile Leu Ser Ala
220          195          200          205
222 ctg gcc ggc ctc ttg ctc ctg gct ttc ctg gca gct tcc act acg cgt 734
223 Leu Ala Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Thr Arg
224          210          215          220
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228 <211> LENGTH: 223
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
232 <400> SEQUENCE: 4
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234 1 5 10 15
236 Leu Val Leu Val Trp Leu Pro Gln Ser Leu Ser Leu Asp Leu Ile Ala
237 20 25 30
239 Tyr Val Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Ile Thr Ala
240 35 40 45
242 Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Glu His Val
243 50 55 60
245 Ser Thr Lys Asp Thr Ile Trp Leu Val Val Ala Phe Ser Asn Ala Ser
246 65 70 75 80
248 Arg Asp Phe Gln Asn Pro Gln Thr Ala Ala Lys Ile Pro Thr Phe Pro
249 85 90 95
251 Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Leu Asp
252 100 105 110
254 Gln Leu Pro Cys Glu Asp Leu Thr Gly Gly Ser Gly Gly Val Pro Val
255 115 120 125
257 Leu Arg Val Gly Asn Asp Phe Gly Cys Tyr Gln Arg Pro Tyr Cys Asn
258 130 135 140
260 Ala Pro Leu Pro Ser Gln Gly Pro Tyr Ser Val Lys Phe Leu Val Met
261 145 150 155 160
263 Asp Ala Ala Gly Pro Pro Lys Ala Glu Thr Lys Trp Ser Asn Pro Ile
264 165 170 175
266 Tyr Leu His Gln Gly Lys Asn Pro Asn Ser Ile Asp Thr Trp Pro Gly
267 180 185 190
269 Arg Arg Ser Gly Cys Met Ile Val Ile Thr Ser Ile Leu Ser Ala Leu

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Input Set : A:\EP.txt

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277 <211> LENGTH: 2744
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279 <213> ORGANISM: Homo sapiens
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
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290 tccagaagct gataaaaaag ctttgggaaa catgaacaaa acattgatga aatgttggaa 180
292 accagttgaa acacagtaaa accaactggg taaaatagga ccacttctct tcatctacac 240
294 tgggatttgt caagaagtga act atg aca ata cat caa ttt ttg cta ctg ttt 293
295                               Met Thr Ile His Gln Phe Leu Leu Leu Phe
296                               1           5           10
298 cta ttc tgg gta tgc ctg cca cat ttc tgc tct cca gaa ata atg ttc 341
299 Leu Phe Trp Val Cys Leu Pro His Phe Cys Ser Pro Glu Ile Met Phe
300                               15          20          25
302 aga agg acg cct gtg cca cag caa aga att tta agt tca cgt gta cca 389
303 Arg Arg Thr Pro Val Pro Gln Gln Arg Ile Leu Ser Ser Arg Val Pro
304                               30          35          40
306 agg agt gat ggc aaa att ctc cat cgt caa aaa cgt ggt tgg atg tgg 437
307 Arg Ser Asp Gly Lys Ile Leu His Arg Gln Lys Arg Gly Trp Met Trp
308                               45          50          55
310 aat caa ttt ttc tta ctt gaa gaa tat aca gga tct gat tat cag tac 485
311 Asn Gln Phe Phe Leu Leu Glu Glu Tyr Thr Gly Ser Asp Tyr Gln Tyr
312                               60          65          70
314 gta ggc aag cta cat tca gac caa gat aaa gga gat gga tca ctc aaa 533
315 Val Gly Lys Leu His Ser Asp Gln Asp Lys Gly Asp Gly Ser Leu Lys
316 75          80          85          90
318 tat atc tta tct gga gat gga gct ggt act ctt ttt att att gat gaa 581
319 Tyr Ile Leu Ser Gly Asp Gly Ala Gly Thr Leu Phe Ile Ile Asp Glu
320                               95          100         105
322 aaa aca ggt gat att cat gcc aca agg cga att gat agg gag gaa aag 629
323 Lys Thr Gly Asp Ile His Ala Thr Arg Arg Ile Asp Arg Glu Glu Lys
324                               110         115         120
326 gcc ttt tat act cta cgc gca caa gct att aac aga aga act ctg agg 677
327 Ala Phe Tyr Thr Leu Arg Ala Gln Ala Ile Asn Arg Arg Thr Leu Arg
328                               125         130         135
330 cca gta gag cca gag tca gag ttt gtg atc aaa att cat gat atc aat 725
331 Pro Val Glu Pro Glu Ser Glu Phe Val Ile Lys Ile His Asp Ile Asn
332                               140         145         150
334 gac aat gag cca acg ttc cca gaa gaa atc tat aca gct agt gtt ccc 773
335 Asp Asn Glu Pro Thr Phe Pro Glu Glu Ile Tyr Thr Ala Ser Val Pro
336 155         160         165         170
338 gaa atg tct gtt gta ggt act tct gtg gtg caa gtc aca gct aca gat 821

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 Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/002,050

DATE: 04/17/2002

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Input Set : A:\EP.txt

Output Set: N:\CRF3\04172002\J002050.raw

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L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:2658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24